AMENDMENTS TO THE CLAIMS

1. (currently amended) A method for identifying a human who has an altered risk for developing coronary stenosis, comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) ~~in said human's nucleic acids as represented by~~ at position 101 of SEQ ID NO:19350 or its complement, wherein a G/G genotype at position 101 of SEQ ID NO:19350 or a C/C genotype at position 101 of its complement ~~the identity of the SNP being G~~ indicates said human is at an increased risk of developing coronary stenosis as compared to a human having an A/A genotype at position 101 of SEQ ID NO:19350 or a T/T genotype at position 101 of its complement ~~at the SNP~~, and an A/A genotype at position 101 of SEQ ID NO:19350 or a T/T genotype at position 101 of its complement ~~the identity of the SNP being A~~ indicates said human is at a decreased risk of developing coronary stenosis as compared to a human having a G/G genotype at position 101 of SEQ ID NO:19350 or a C/C genotype at position 101 of its complement ~~at the SNP~~.

2. - 5. (canceled)

6. (currently amended) The method of claim 1 in which the testing is performed ~~identity of the SNP is determined~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

7. - 24. (canceled)

25. (currently amended) The method of claim 1, wherein the SNP ~~to be determined~~ is located at position 79090 of SEQ ID NO: 12227.

26. (currently amended) The method of claim 1, wherein the SNP ~~to be determined~~ is located in the LPA gene.

27. (currently amended) The method of claim 1, wherein the testing is performed ~~identity of the SNP is determined~~ by using a set of detection reagents comprising the oligonucleotide sequences of SEQ ID NO: 68222, SEQ ID NO: 68223, and SEQ ID NO: 68224.

28. (currently amended) A method for identifying a human who has an increased risk for developing coronary stenosis, comprising testing nucleic acid from said human for the presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) ~~in said human's nucleic acids as represented by~~ at position 101 of SEQ ID NO:19350 or its complement, wherein a G/G genotype at position 101 of SEQ ID NO:19350 or a C/C genotype at position 101 of its complement ~~the identity of the SNP being G~~ indicates said human is at an increased risk of developing coronary stenosis as compared to a human having an A/A genotype at position 101 of SEQ ID NO:19350 or a T/T genotype at position 101 of its complement ~~at the SNP~~.

29. (currently amended) The method of claim 28 in which the testing is performed ~~identity of the SNP is determined~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

30. (currently amended) The method of claim 28, wherein the SNP ~~to be determined~~ is located at position 79090 of SEQ ID NO: 12227.

31. (currently amended) The method of claim 28, wherein the SNP ~~to be determined~~ is located in the LPA gene.

32. (currently amended) The method of claim 28, wherein the testing is performed ~~identity of the SNP is determined~~ by using a set of detection reagents comprising the oligonucleotide sequences of SEQ ID NO: 68222, SEQ ID NO: 68223, and SEQ ID NO: 68224.

33. (currently amended) A method for identifying a human who has a decreased risk for developing coronary stenosis, comprising testing nucleic acid from said human for the

presence or absence ~~determining the identity~~ of a single nucleotide polymorphism (SNP) ~~in said human's nucleic acids as represented by~~ at position 101 of SEQ ID NO:19350 or its complement, wherein an A/A genotype at position 101 of SEQ ID NO:19350 or a T/T genotype at position 101 of its complement ~~the identity of the SNP being A~~ indicates said human is at a decreased risk of developing coronary stenosis as compared to a human having a G/G genotype at position 101 of SEQ ID NO:19350 or a C/C genotype at position 101 of its complement ~~at the SNP~~.

34. (currently amended) The method of claim 33 in which the testing is performed ~~identity of the SNP is determined~~ by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

35. (currently amended) The method of claim 33, wherein the SNP ~~to be determined~~ is located at position 79090 of SEQ ID NO: 12227.

36. (currently amended) The method of claim 33, wherein the SNP ~~to be determined~~ is located in the LPA gene.

37. (currently amended) The method of claim 33, wherein the testing is performed ~~identity of the SNP is determined~~ by using a set of detection reagents comprising the oligonucleotide sequences of SEQ ID NO: 68222, SEQ ID NO: 68223, and SEQ ID NO: 68224.

38. (currently amended) The method of claim 1, further comprising providing a report of the presence or absence ~~identity~~ of said SNP.

39. (previously presented) The method of claim 1, further comprising providing a report of said human's altered risk for developing coronary stenosis.

40. (previously presented) The method of claim 39, wherein the altered risk is an increased risk for developing coronary stenosis.

41. (previously presented) The method of claim 39, wherein the altered risk is a decreased risk for developing coronary stenosis.

42. (currently amended) The method of claim 39, wherein the report further shows the presence or absence ~~identity~~ of said SNP.

43. (currently amended) The method of claim 42, wherein ~~the identity of~~ said SNP comprises said G/G or said C/C genotype ~~is G or its complement thereof~~, and wherein the report indicates said human has an increased risk of developing coronary stenosis.

44. (currently amended) The method of claim 42, wherein ~~the identity of~~ said SNP comprises said A/A or said T/T genotype ~~is A or its complement thereof~~, and wherein the report indicates said human has a decreased risk of developing coronary stenosis.

45. (previously presented) The method of any one of claims 38-44, wherein the report is in paper form or computer readable medium form.

46. (new) The method of claim 1, wherein said nucleic acid is a nucleic acid extract from a biological sample from said human.

47. (new) The method of claim 46, wherein said biological sample is blood, saliva, or buccal cells.

48. (new) The method of claim 46, further comprising preparing said nucleic acid extract from said biological sample prior to said testing step.

49. (new) The method of claim 48, further comprising obtaining said biological sample from said human prior to said preparing step.

50. (new) The method of claim 1, wherein said testing step comprises nucleic acid amplification.

51. (new) The method of claim 50, wherein said nucleic acid amplification is carried out by polymerase chain reaction.

52. (new) The method of claim 28, further comprising correlating the presence of said G/G genotype or said C/C genotype with an increased risk for developing coronary stenosis.

53. (new) The method of claim 52, wherein said correlating step is performed by computer software.

54. (new) The method of claim 28, further comprising correlating the absence of said G/G genotype or said C/C genotype with no increased risk for developing coronary stenosis.

55. (new) The method of claim 54, wherein said correlating step is performed by computer software.

56. (new) The method of claim 33, further comprising correlating the presence of said A/A genotype or said T/T genotype with a decreased risk for developing coronary stenosis.

57. (new) The method of claim 56, wherein said correlating step is performed by computer software.